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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:		Examiner # :	Date:
Art Unit:	Phone Number 30	Serial Number:	•
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If more than one search i	s submitted, please	prioritize searches in order of n	eed.
Please provide a detailed stateme Include the elected species or str	ent of the search topic, and uctures, keywords, synonyon ony terms that may have a s	******************************** describe as specifically as possible the sul ms, acronyms, and registry numbers, and pecial meaning. Give examples or releva aims, and abstract.	bject matter to be searched.
Title of Invention:	· · · · · · · · · · · · · · · · · · ·		
Inventors (please provide full r	names):	·	
Earliest Priority Filing Date	·		
For Sequence Searches Only Pla appropriate serial number.	ease include all pertinent info	rmation (parent, child, divisional, or issued p	patent numbers) along with the
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
PRINTS;
                                                                                                   PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
EMBL; BC001125; AAH01125.1; -.
EMBL; BC008848; AAH08848.1; -.
EMBL; BC020800; AAH20800.1; -.
HSSP; B23284; 1CYN.
                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
-:- SIMILARITY).
-:- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.
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TISSUE*PROSTATE;
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Strausberg R.;
Submitted (MAY-2001)
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Homo saplens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                   Pfam; PF00160;
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F00160; pro_isomerase; PR00153; CSAPPISMRASE
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-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
EMBL; AF071225; AAC25590.1; -.
HSSP; P23284; ICYN.
InterPro; IPR002130; CSA_PPIASE.
Pfam; PF00160; Pr0_150Merrase; 1.
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01-NOV-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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PROSITE; PS50072; CSA_PPIASE_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1998) to the EMBL/GenBank/DDBJ -1- FUNCTION: PPIASES ACCELERATE THE FOLDING C
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Kainer D.B., Doris P
"Cyclophilin B.";
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100.08;
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                                                                                                                                                                                                                                                                                       Score 98;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                            02408DFA7157218C CRC64;
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6.4e-92;
hes 0;
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                                                                                                                                                                                                                                                                                                         Length 208;
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R Fleischmann W., Gassterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Gustincich S., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Wilming L.,

RA Suzuki H., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

**Functional amoutstich of a full-length mouse CNA Collection **.
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                                                                                                                                                                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                                                                                                          Query Match
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O9DCY1; O1-JUN-2001 (TIEMBLrel 17, Created)
O1-JUN-2001 (TIEMBLrel 17, Last sequence update)
O1-JUN-2002 (TIEMBLrel 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002130; CSA_PPIase. Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AK002357; BAB22036.1; -. EMBL; BC013061; AAH13061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M.,
Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yan
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T.,
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=KIDNEY; MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                               54 FGLEGKTVPKTVDNFVALATGEKGEGYKNSKEHRVIKDEMIQGGDETRGDGTGGKSIYGE 113
                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                        RFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKT 151
                                                                                                                                                                      RFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKT 159
                                                                                                                                                                                                                                               FGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGE
                                                                                                                                                                                                                                                                                                                                            Similarity
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Pred. No.
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S., Yamanaka
Saito
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Q01490; Q01490; 01-NOV-1998 01-NOV-1998 01-DEC-2001

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Best Local S
Matches 37
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01-JUN-2002 (TEMBLIEL 21, L
Cyclophilin-like peptidyl prol
5:2.1.8).
MOÎ. Gen. Genet. 266:537-545(2001).
EMBL: AY005867; AAF98447.1;
InterPro; IPR0001310; CSA_PPIASE.
InterPro; IPR000886; ER_target.
Pfam. PF00160; Pro_1somerase; 1.
PROSITE; PS00170; CSA_PPIASE_1; UNKNOWN_1.
PROSITE; PS00072; CSA_PPIASE_2; 1.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8X166;
Q8X166;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
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-i- FUNCTION: PPIASES ACCELERATE THE POLDING OF PROTEINS.
-i- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLICOPETIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Chytridiomycota
Neocallimasticaceae; Orpinomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
Isomerase; Rotamase; Signal; Cyclosporin; Endoplasmic reticulum.
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InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U17900; AAD04195.1; HSSP; P23284; ICYN.
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-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen H., Li X.-L., Ljungdahl L.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus niger.
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Asperg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                   Aspergillus niger and contains signal HEEL.";
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"The foldase CYPB is a component of the
                                                                                                                                                                                                                                                                                                               signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERF 115
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37; Conser
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ilarity 100.0%;
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prolyl cis-trans isomerase
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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PREVENT SECRETION FROM ER
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A5748C94305B8BE0 CRC64;
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Best Local
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Q29278;
Q1-NOV-1996
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01-MAY-1999
01-MAY-1999
01-MAR-2002
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Sus scrofa (Pig).
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EMBL; F14628; CAA23162.1; -.
HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00160; pro_isomerase; PRINTS; PR00153; CSAPPISMRASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96327607; PubMed=8672129;
Winteroe A.K., Fredholm M., Davie
                                                                                                                                                                                                                                                                                                                                                                                     094190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50072; CSA_PPIASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
                   cyclophilin B.";
Fungal Genet. Bi
-i- FUNCTION: PP
                                                                        SEQUENCE FROM N.A.
MEDIINE-99343878; PubMed-10413615;
JOSeph J.D., Heitman J., Means A.R.;
"Molecular cloning and characterization
                                                                                                                                                                                                Eurotiales; Trichocomaceae; E
                                                                                                                                                                                                                                          Emericella nidulans
                                                                                                                                                                                                                                                                CYPB
                                                                                                                                                                                                                                                                                  Cyclophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002130; CSA_PPlase
                                                                                                                                                                          NCBI_TaxID=162425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 WLDGKHVVFGKVLEGMEVVRKVESTKTD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 WLDGKHVVFGKVLEGMEVVRKVESTKTD
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28; Conser
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TrEMBLrel.
TremBLrel.
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                   Biol. 27
PPIASES
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                                          27:55-66(1999)
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                   ACCELERATE THE
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Last annotation updat
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Pred. No.
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Last annotation update)
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3e-21;
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                      PROTEINS
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RESILY

OPERATOR

ACCOMMENT

REPARATOR

OPERATOR

OPERAT
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Best Local
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InterPro; IPR000886; ER_target.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE_1; PR0517E; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS00072; CSA_PPIASE_2; 1.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
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01-MAY-1999
01-MAY-1999
01-MAR-2002
       01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE BONDS IN OLIGOPEPTIDES.

1 SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
EMBL; AF0798071; AAC64933.1;

HSSP; P05092; ZCPL.
Interpro; IPR002130; CSA_PPIASE.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS0072; CSA_PPIASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee Y.K., Hong C.B., Shu Y., Lee I.K.;

"Isolation of a cDNA Clone for Cyclophilin from Griffithsia japonica and Structural Comparison of Cyclophilins.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY SIMILARITY).
                                                      Q8X0S3;
                                                                      Q8X0S3
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Rhodophyta; Florideophyceae; Griffithsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9ZT54
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-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY. BMBL; AF107254; AAD17998.1; -.
HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-83288
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                                                                                                                                                                                                                                                                                                                                                                               Isomerase;
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                                                                                                                                                                                                            QGGDFTRGDGTGGKSIYGE 113
                                                                                                                                                                                QGGDFTRGDGTGGKSIYGE
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                                                                                                                                                                                                                                                                                          Similarity
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28; Conserv
  (TrEMBLrel.
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9 (TrEMBLrel.
2 (TrEMBLrel.
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                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.5%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVITY: CIS-TRANS ISOMERIZATION
                                                                                                                                                                                                                                                                                                                                                       17254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23406 MW; SA4DCFAEBE529DFA CRC64;
                                                                                                                                                                                                                                                                                        9.1%;
    20,
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Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                        Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                     7752D5C2051FD92E CRC64;
                                                                                                                                                                                                                                                                  Mismatches
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                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162
                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ceramiales; Ceramiaceae;
                                                                 AA
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                                                                                                                                                                                                                                                                                                          Length 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF PROLINE IMIDIC
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RESULT 10
Q917V3
ID Q917V
AC Q917V
D1 O1-MA
D7 01-MA
D7 01-MA
D7 01-D1
GN CG28!
GN CGCAR
GN CGCAR
GN C
RC STRAIN-BERKELEY;
RX MEDLINE-20196006: PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Ashburner M., Henderson S.N.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Bronstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Andrews-Pfannkoch C., Baldwin D.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Dayenport L.B., Davies P.,
RA Geblos B., Delcher A., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dukov B.C., Dunn P.,
RA Golder C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guann P., Harris M.,
RA Hostin D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Howland T.J., Wei M.-H., Ibeyawam C.,
RA Jalaii M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lia Y., Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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Best Local
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Submitted (JAN-2002) to the EMBL/GenBank/DDB.
EMBL, KL670011; CAD21421.1; -
Interpro; IrR002130; CSA_PPIASE.
Pfam; PF00150; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIASE_1; UNKNOWN_1.
PROSITE; PS00170; CSA_PPIASE_2; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
SEQUENCE 207 AA; 22557 MW; AA0B42D3A8D9E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q917V3;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2002)
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Sordariales: Sordariaceae: Neurospora.
NCBI_TaxID=5141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 19,
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N-2002) to t
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100.0%; Pred. No. 5.
tive 0; Mismatches
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H.W., Mannhaupt G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Q25093
ID Q2509
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DT Q1-NC
DT Q1
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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Ra Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Ventor E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.M., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RY The genome sequence of Drosophila melanogaster.";
RT The genome sequence of Drosophila melanogaster.";
                                                                                  Query Match
Best Local
                                                    Matches
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PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS50072; CSA_PPIASE_2;
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Q25093;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hirudo medicinalis (Medicinal leech).
Eukaryota: Metazos: Annelida; Clitellata: Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TREMBLICEL 01, 01-NOV-1996 (TREMBLICEL 01, 01-MAR-2002 (TREMBLICEL 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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InterPro; IPR002130; CSA PPIase.
Pfam; PF00160; Pro_isomerase; 1.
PRINTS; PR00153; CSA_PPISMASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                EMBL; U36797;
HSSP; P05092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "CDNA libraries from identified neurons.";
Proc. R. Soc. Lond., B. Biol. Sci. 263:57-62(1996).
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96165729; PubMed-8587897;
Korneev S., Blackshaw S.E., Kaiser K., Davies J.A.;
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95 QGGDFTRGDGTGGKSIYG 112
                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PETTIDE BONDS IN OLIGOPEPTICES.
SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
L; U36797; AAB01531.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMANAGKDTNGSQFFITT 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / G.,
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IPR002130; CSA_PPIase.
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                                                       Conservative
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Pred. No. 3.2e-1
                                                          0
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Pred. No.
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                                                             Mismatches
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Q9W227;
Q1-MAY-2000
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amenatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Adbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow D. B., Baldwin D.,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000
01-MAR-2002
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CG2852.
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Pfam; PF00160; pro_isomerase;
PRINTS; PR00153; CSAPPISMRASE;
PROSTTE; PS000170; CSA_PPIASE_1
PROSITE; PS50072; CSA_PPIASE_2
                                                                                                                                                           HSSP; P23284; 1CYN.
FlyBase; FBgn0034753; CG2852
                                                                                                                                                                                                                          PEPTIDE BONDS IN OLIGOPEPTIDES.
-!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY BENBL; AE003458; AAF46873.1; -.
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0 (TrEMBLrel. 13,
2 (TrEMBLrel. 20,
                                                                                               IPR002130; CSA_PPIase
0160; pro_isomerase; 1
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Best Local Similarity 100
Matches 18; Conservative
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O93826, O9
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Eukaryota; Fungi; Ascomycota;
Onygenales; Arthrodermataceae;
                                                                    Arthroderma benhamiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00160; IPR002130; CSA_PPIASE.
Pfam; PF00160; pro_lsomerase; 1.
PRINTS; PR00153; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
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A peptidyl-prolyl cis/trans-isomerase (cyclophilin G) in secretory granules.",

J. Biol. Chem. 272:28615-28621(1997).

-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
ROLL IN MAINTAINING THE CONFORMATIONAL INTEGRITY OF S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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-1- TISSUE SPECIFICITY: HEMOCYTE LARGE SECRETORY GRANULES.
-1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
EMBL; AB002814; BAA23764.1; -.
HSSP; P22284; ICVN.
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Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; xiphosura;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 SMANAGKDTNGSOFFITT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION
PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIYGERFPDENFKLKHYG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIYGERFPDENFKLKHYG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 AA;
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205 AA;
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                          Ascomycota; Pezizomycotina; Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220
24198 MW;
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Last sequence up
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Pred. No.
                                                                                                                                                                                                                                                                                   PRT;
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5.7e-10;
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Query Match
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Matches 17
                                                                  HSSP; P05092; ZCPL.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS00072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                   015729
015729;
01-JAN-1998
01-JAN-1998
01-JAR-2002
                                                                                                                               -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY EMBL; AF017993; AAB86601.1; -. HSSP; P05092; 2CPL.
                                                                                                                                                                                                    "Cloning, characterization and functional expression of Entamoeba histolytica."; Mol. Biochem. Parasitol. 107:219-225(2000).

"I FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTE
                                                  SEQUENCE
                                                                                                                                                                  -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                 Ostoa-Saloma P.,
                                                                                                                                                                                                                                                                          MEDLINE=20243663; PubMed=10779598
                                                                                                                                                                                                                                                                                        STRAIN-HM1: IMSS;
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5759
                                                                                                                                                                                                                                                                                                                                     Entamoeba histolytica.
Eukaryota; Entamoebidae;
                                                                                                                                                                                                                                                                                                                                                                 CYPI
                                                                                                                                                                                                                                                                                                                                                                          Cyclophilin.
                                                                                                                                                                                                                                                     Laclette J.P.;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: BELONGS TO BMBL; AB019518; BAA34384.1; HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20174741; PubMed-10711599; Kano R., Nakamura Y., Watanabe S., Tsujimoto H., Hasegawa A.; "Characterization of the cyclophilin of Trichophyton mentagrophytes."; Microbiol. Immunol. 44:51-56(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002130; CSA_PPIAse. Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-VUT-77011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 SMANAGKDTNGSQFFITT 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=63400;
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               Similarity
                                                 Rotamase.
167 AA;
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   Conservative
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                                                 18139 MW;
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                                                                                                                                                                                                                                                                                                                                     Entamoeba
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            Score 17;
Pred. No.
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Last sequence update)
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Pred. No.
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                                                DBA23FE5BB3290B2 CRC64;
                                                                                                                                                                                                                                                             Petrossian P., Herion P.,
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 167
            DB 5; Lo
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5.9e-1
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                       Length 167;
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  Indels
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                                                                                                                                                                                                                                     of a cyclophilin
                                                                                                                                                                                                                                                             Landa A.,
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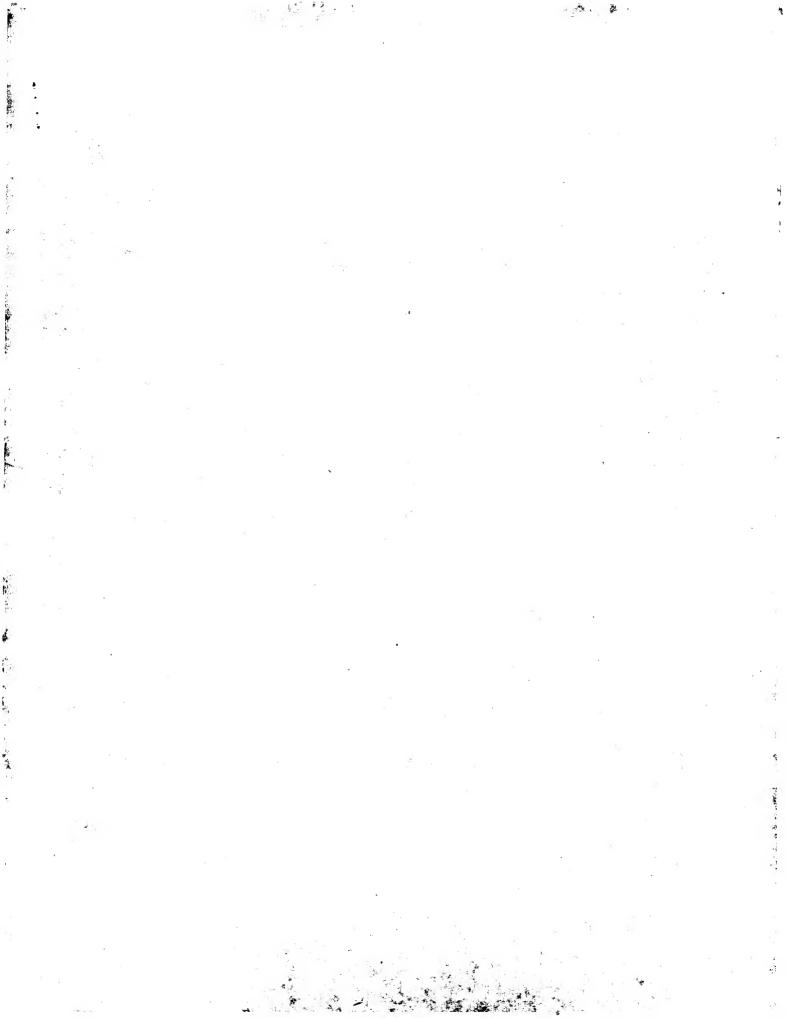
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Maximum DB seq length: 2000000000
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208
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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22	29	64	98	137	183	203	208	208	208	Score		
10.6	13.9	30.8	47.1	65.9	88.0	97.6	100.0	100.0	100.0	Match))	
83	212	64	183	166	163	211	291	291	216	Match Length DB		
22	21	23	22	21	22	22	23	21	22	B		
AAM24287	AAY92048	AAU99181	AAG65274	AAG00090	AAG65273	AAB73302	ABP41842	AAB43878	AAB73301	ID		SUMMARIES
Human EST encoded	A. niger peptidyl-	Partial human pert	Haematopoietic ste	Human secreted pro	Haematopoietic ste	Human cyclophilin	Human ovarian anti	Human cancer assoc	Human cyclophilin	Description		

4 U	44	43	42	41	40	39	38	37	36	ω	34	ω ω	32	31	0	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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184	176	169	165	165	165	164	164	163	163	162	152	145	145	145	114	106	754	737	236	228	125	250	214	193	183	183	58	58	212	185	185	180	205	120
23	21	23	22	21	19	22	01	22	12	21	21	16	16	12	22	22	23	22	21	21	21	22	22	23	22	21	22	22	14	22	22	19	22	22
ABP41129	AAG44156	ABP42929	AAU01195	AAG03831	AAW56028	AAG65275	AAP90431	AAG65276	AAR13726	AAG44157	AAG08983	AAR72961	AAR72917	AAR10763	AAB64736	ABG27275	AAE24596	ABG10283	AAG18025	AAG18026	AAG18027	ABG23480	ABG23479	ABP42003	ABB66236	AAB56701	ABG29318	ABG12991	AAR32353	AAG65278	AAG65277	AAW80784	929	ABB67378
	Arabidopsis thalia		Human cyclophilin	Human secreted pro	Calcineurin protei	ic	Cyclophilin. Homo	Haematopoietic ste	Bovine cyclophilin	Arabidopsis thalia	Sisc	per		ne	Gene 14 human secr	Novel human diagno	SR-cy				opsis	human	Novel human diagno	Human ovarian anti	ס		Novel human diagno	Novel human diagno			Haematopoietic ste	Α.	Drosophila melanog	Drosophila melanog

ALIGNMENTS

			KW Human cyclo			AC AAB73301;	ID AAB73301 st	AAB73301	RESULT 1	
prostate cancer: digantism: acromedaly: hypern	muscle wasting; osteoporosis; HIV infection; b	genic function modulator; immunosup	Human cyclophilin B; CypB; prolactin-binding;	Human cyclophilin B (CypB).	22-MAY-2001 (first entry)		AAB73301 standard; protein; 216 AA.			

growth hormone-binding;
ppression; short stature;
preast cancer;

Homo sapiens.

W0200113113-A1

22-FEB-2001

10-AUG-2000; 2000WO-US21789

19-AUG-1999; 9905-0149752

(UYPE-) UNIV PENNSYLVANIA

Clevenger CV, Rycyzyn MA;

WPI; 2001-211249/21.

Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin

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ARESULT 2
ANAB43878
ID AAB4
AC AAB4
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Matches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                              dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interaction of cyclophilin B with a somatolactogenic hormone, is useful for inhibiting somatolactogenic function in the animal. A composition comprising cyclophilin B is useful in the treatment of immunosuppression, in the treatment of short stature, muscle wasting and osteoporosis. A composition comprising cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful for treating HIV infection, breast and prostate cancer, gigantism/acromegaly, and hyperprolactinaemia. The present sequence represents human cyclophilin B.
                                                                                                                                                                                                                                                                                                                                                                   Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B with somatolactogenic hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB43878 standard;
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                                    WO200055350-A1
                                                                                                  Homo sapiens.
                                                                                                                                                                 neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer associated protein sequence SEQ ID NO:1323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLKHYGPGWYSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTD
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                                                                                                                                                                 disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                    drug
                                                                                                                                                                    screening
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Pred. No. 4.9e-194;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovacular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coaquiant; nootropic; vasotropic; antipsoriattic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating cameliorating medical conditions and diagnosing pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing {
m e.g.} cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in AAB43398 to AAB44239. The proteins can have activities based on tissues and cells the genes are expressed in Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 1974-1975; 2352pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-2000;
                                                       22-AUG-2002
                                                                                           ABP41842;
                                                                                                                               ABP41842 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC78087.
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                                                                                                                                                                                                                                                                                              204
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                                                                                                                                                                                                                                                                                                                                                                                                                                            84 MKYLLAAALIAGSVFFLLLPGPSAADEKKKGPKYTVKVYFDLRIGDEDVGRVIFGLFGKT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKYLLAAALIAGSVFFLLLPGPSAADEKKKGPKVTVKVYFDLRIGDEDVGRVIFGLFGKT 60
                                                                                                                                                                                                                                               SRDKPLKDVIIADCGKIEVEKPFAIAKE 208
                                                                                                                                                                                                                                                                                                                                                                      VPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENF
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                                                                                                                                                                                                                         SRDKPLKDVITADCGKIEVEKPFATAKE
                                                                                                                                                                                                                                                                                                                                  KLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTD
                                                                                                                                                                                                                                                                                                KLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US05882
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                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 208; DB 21; 100.0%; Pred. No. 6.4e-194;
                                                                                                                                 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                               B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
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                                                                                                                                                                                                                                                                                                                                    180
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Human ovarian

antigen HTFML39,

SEQ

ID NO: 2974

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CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also CC encompasses polypeptides 90% identical and polynucleotides 95% identical comprising human ovarian antigens (ABP41054-CC encompasses polypeptides 90% identical and polynucleotides 95% identical comprising human ovarian antigen active to the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen comprising human ovarian antigen active yearian antigen polynucleotides against human ovarian antigens, and the use of polynucleotides, antibodies against human ovarian antigens, and the use creating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, complexated covary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., congenital and acquired immunedisorders, conditions (e.g., mastitis, ophoritis and complexated disorders (e.g., anaemia), cardiovascular disorders, conditions (e.g., mastitis, ophoritis and crespiratory disorders (e.g., anaemia), cardiovascular disorders, conditions (e.g., congenital and acquired immunedisorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which complete ovarian antigen expression or activity. The polynucleotides may disorders (e.g., anaemia), cardiovascular disorders and the complete ovarian antigen of the invention.

CC useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention.

CC useful in disease data for this patent did not form part of the printed constitution, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; pCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-147878/19
N-PSDB; ABQ54919.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gynaecological; reproductive.
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1 MKVLLAAALIAGSVFFLLLPGPSAADEKKKGPKVTVKVYFDLRIGDEDVGRVIFGLFGKT

Matches

Similarity

100.0%; 0;

Score 208; DB 23; Pred. No. 6.4e-194; Mismatches

Length Indels

0

Gaps 60

0

Conservative

Sequence

291

A

at ftp.wipo.int/pub/published_pct_sequences

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The invention relates to a composition for modulating somatolactogenic CC function, comprising cyclophilin B (CYPB), a mutant of cyclophilin B CC (particularly a CypB mutant in which residues 2-12 of the mature protein CC are absent) or an inhibitor of the interaction of cyclophilin B with a CC somatolactogenic hormone (e.g., prolatin, growth hormone). The invention CC also relates to a method of identifying inhibitors of somatolactogenic control of somatolactogenic functions using CypB and a somatolactogenic hormone, and a method for CC diagnosing diseases associated with abnormal somatolactogenic functions by assessing CypB levels in a sample from a patient. Cyclophilin B is CC useful for augmenting somatolactogenic function in the animal, and CC cyclophilin B mutant or a composition comprising an inhibitor of the interaction of cyclophilin B with a somatolactogenic hormone, is useful CC in the interaction of cyclophilin B with a somatolactogenic function in the animal. A composition comprising cyclophilin B mutant or a composition comprising cyclophilin B with a somatolactogenic cyclophilin B with a somatolactogenic cyclo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
AAB73302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition for modulating somatolactogenic function, comprises cyclophilin B, its mutant or an inhibitor of interaction of cyclophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cyclophilin B; CypB; prolactin-binding; growth hormone-binding; somatolactogenic function modulator; immunosuppression; short stature muscle wasting; osteoporosis; HIV infection; breast cancer; pigantism; acromegaly; hyperprolactinaemia; prostate cancer; gigantism; acromegaly; hyperprolactinaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page -; 21pp; English.
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RESULT 5
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Best Local (
                                             Query Match
Best Local Similarity
Matches 183; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                       Haematopoietic stem cell proliferation dyshaemopoiesis; cancer; human; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                  The present invention provides a proliferation agent for haematopoietic stem cells, which contains cyclophilin. This may be used in the treatment of dyshaemopolesis in radiotherapy and chemotherapy of various haematopoletic organ diseases and cancers. The present sequence is a human protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                         JP2001163798-A
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                                                                                              Sequence
                                                                                                                                                                                            Claim
                                                                                                                                                                                                                              Proliferation
                                                                                                                                                                                                                                                     WPI; 2001-592517/67.
                                                                                                                                                                                                                                                                           (KANF ) KANEKA
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                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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           DEKKKGPKUTVKYYFDLRIGDEDVGRVIFGLFGKTVPKTVDNFVALATGEKGFGYKNSKF
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 DEKKKGPKVTVKVYFDLRIGDEDVGRVIFGLFGKTVPKTVDNFVALATGEKGFGYKNSKF
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                                                                                                                                                                                         Page 13-14; 19pp; Japanese.
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                                                                                               183 AA;
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ilarity 100.0%;
Conservative
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                                         88.0%; Uz
100.0%; Pr/
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Pred. No.
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. 3.5e-189;
                                                         DB 22;
8.8e-170;
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RESULT 6
AAG00090
ID AAG0
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                         δÃ
                                                         Matches 137;
                                                                                  Query Match
                                                                                                                                  The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30' different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA librarise. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG00090;
                                                                                                                                                                                                                                                                                                                                    Claim 13; SEQ ID 4171; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-500381/45
N-PSDB; AAC00096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                               Sequence
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                                                                      Local Similarity
AKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENFKLKHYGPGWVSMANAGKDTNGSQFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITTVKTAWLDGKHYVFGKVLEGMEVVRKVESTKTDSRDKPLKDVIIADCGKIEVEKPFAI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRVIKDEMIQGGDETTRGDGTGGKSIYGEREPDENEKLKHYGPGWVSMANAGKDTNGSQFF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTDSRDKPLKDVIIADCGKIEVEKPFAI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208
                                                                                                               166 AA;
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome
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                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mapping.
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                                                                      Score 137;
Pred. No.
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                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Giordano
                                                                      DB 21;
4.5e-125;
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                                                                                    Length
                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                 procedures
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RESULT 7
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AAU99181
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a proliferation agent for haematopoietic stem cells, which contains cyclophilin. This may be used in the treatment of dyshaemopoiesis in radiotherapy and chemotherapy of various haematopoietic organ diseases and cancers. The present sequence is a murine protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haematopoietic stem cell proliferation dyshaemopoiesis; cancer; human; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG65274 standard; protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haematopoietic stem cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG65274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proliferation agent for hematopoietic stem cell containing cyclophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-592517/67
             Partial human perturbagen F802
                                            24-SEP-2002 (first entry
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KANF ) KANEKA CORP
                                                                                                       AAU99181 standard; Protein; 64 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 KLKHYGPGWVSMANAGK 145
                                                                                                                                                                                                            114 REPDENEKLKHYGPGWYSMANAGKDTNGSQFFITTYKT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                68
                                                                                                                                                                                                                                           29
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                                                                                                                                                                                                                                           FGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGE 88
                                                                                                                                                                                                                                                                       FGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLKHYGPGWVSMANAGK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENF 128
                                                                                                                                                                                RFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKT 126
                                                                                                                                                                                                                                                                                                      98;
                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 14; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                               183 AA;
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0345542
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                                                                                                                                                                                                                                                                                                                   47.1%;
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                                                                                                                                                                                                                                                                                                                   Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agent related murine protein
                                                                                                                                                                                                                                                                                                                   DB 22;
4.2e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cyclophilin;
                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                Length 183
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61 KLKH

64

121 KLKH 124

Matches

64; Similarity

Conservative

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Mismatches

Gaps

0;

30.8%;

Score 64; Pred. No.

DB 23; 1.9e-54; 0;

Length 64 Indels

Sequence

64 AA;

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CC Also included are the polynucleotide, preparing an RA pathway related to polyneptide, a composition pair identified by a method utilising the polynucleotide, preparing an RA pathway related CC polypeptide, screening (M) putative RA-related therapeutics. by exposing CC the RA pathway polypeptide, to a number of agents, and recovering a cc subpopulation of disrupting agents which competitively displace the CC polypeptide from the target, where the disrupting agents are putative RA-related therapeutics. Also include are an isolated RA pathway polypeptide cc comprising PAT1 (a kinesin light chain-related protein) polypeptide cc comprising PAT1 (a kinesin light chain-related protein) polypeptide comprising the gene therapy vector. The RA pathway polypeptide comprising the gene therapy vector. The RA pathway polypeptide comprising the gene therapy vector. The RA pathway polypeptide is objective, by exposing the polypeptide in vitro to putative target conspersion of identifying a polypeptide in vitro to putative target conspersion in the polypeptide in vitro to putative target conspersion in the polypeptide is also useful for treating consersion in the polypeptide is also useful for treating cancer, demanding cancer, Karposi's sarcoma, construction patatic, pancreatic cancer, neuroblastoma, renal cancer, covarian cancer, demanticis, hyperkeratosis, eczema, Darier's disease, concer is a partial human perturbagen f802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Retinoic acid pathway; RA; retinoid; lung cancer; Rarposi's sarcoma; breast cancer; panereatic cancer; neuroblastoma renal cancer; ovarian cancer; disease; hyperkeratosis; eczema; barier's disease; Reiter's disease; psoriasis; gene therapy; F797; acute promyelocytic leukaemia; APL; Perturbagen; R3; F802; F820; yeast two-hybrid assay; PATI; kinesin light chain-related protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polypeptide (I) with retinoic acid (RA) pathway activity, comprising a polypeptide sequence of Perturbagen (phenotypic probe) R3, Perturbagen R802, Perturbagen R820, their biologically active modifications, or biologically active fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide with retinoic acid pathway activity, especially of perturbagens R3, F802 and F820 for identifying a cellular targ interacts with the polypeptide and for therapeutic purposes \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 13a; 131pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200240719-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BT,
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RESULT 10
AAM24287
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                                                                                                                                                 Query Match
Best Local S
Matches 29
                                                                                                                                                                                                                   This sequence shows Aspergillus niger cyclophilin-like peptidyl prolyl clis-trans isomerase (CYPB). CYPB is capable of catalyzing the cis-trans isomerization of a peptide bond on the N-terminal side of proline residues in polypeptides. CYPB are useful in methods for increasing the yield of secreted polypeptides from cells. The secreted polypeptides may be enzymes (such as chymosin, thaumatin or alpha-galactosidase) that can be used in food processing, a pest toxin, adenosine diphosphate (ADP)-glucose pyrophosphorylase, a glucanase or beta-1,4-endoglucanase.
            AAM24287;
                                   AAM24287 standard;
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                        Claim 13; Page 47-48; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                         New peptidyl prolyl cis-trans isomerase, designated CYPB, from Aspergillus niger, useful in methods for increasing the yield of secreted polypeptides, such as enzymes used in food processing, from
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-293167/25.
N-PSDB; AAA08772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclophilin-like peptidyl prolyl cis-trans isomerase; CYI food processing; Endoplasmic_retention signal; cis-trans
                                                                                                                                                                                                                                                                                                                                                                     cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DANI-) DANISCO AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein secretion; toxi beta-1,4-endoglucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A. niger peptidyl-prolyl cis-trans isomerase (CYPB)
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                                                                                              85 FHRVIKDEMIQGGDFTRGDGTGGKSIYGE 113
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocessing; Endoplasmic retention signal; cis-trans isomerization; secretion; toxin; ADP-glucose pyrophosphorylase; glucanase;
                                                                                                                                                                                                    212 AA;
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Madrid SM
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24..212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                   Protein;
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                                                                                                                                                              13.9%;
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                                    83
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                                                                                                                                                              Score 29;
Pred. No.
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                                                                                                                                                 Mismatches
                                                                                                                                                DB 21;
, 6.1e-20;
ches 0;
                                                                                                                                                                       Length 212;
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RESULT 11
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Best Local :
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03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                     Drosophila
                    WO200171042-A2
                                           Drosophila melanogaster
                                                                   pharmaceutical.
                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                             26-MAR-2002
                                                                                                                                                                          ABB67378 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
                                                                                                                                                   ABB67378;
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 1183–1184; 1275pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for treatment of diseases, antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-476164/51.
N-PSDB; AAH98946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                 28 KKKGPKVTVKVYFDLRIGDEDV
                                                                                                                                                                                                                                                        28 KKKGPKVTVKVYFDLRIGDEDV
                                                                                                                                                                                                                                                                                            Local Similarity
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Drmanac RA,
                                                                                                  melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                              83 AA;
                                                                                                                                                                                                                                                                               10.6%; Score 22; ilarity 100.0%; Pred. No. Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0491404.
2000US-0617746.
2000US-0631451.
2000US-0663870.
                                                                                                                           (first entry)
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lan T;
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          N-PSDB; ABL03400
                   WPI; 2001-656860/75
                                                                             23-MAR-2000;
11-JUL-2000;
                                                          (PEKE ) PE CORP NY.
                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                              27-SEP-2001
                                                                                                                                                  WO200171042-A2
                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                              Drosophila; developmental biology; cell
                                                                                                                                                                                                                      Drosophila
                                                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                                               ABB59297 standard;
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic a genes from Drosophila interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                            131 SMANAGKDTNGSQFFITT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                                                SMANAGKDTNGSQFFITT 56
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                                       JC,
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2000US-0614150
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2000US-0614150
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Pred. No.
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Russell
                                                                                          disorders,
                                                                                          Bisphosphonate binding protein - used disorders, including bone metabolism,
                                                                                  metastases, and
                                                                                                                                                                                                                       14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                       Dictyostelium,
bisphosphonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The Invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL0140-ABL16175) and the encoded proteins
                                                                                                                            N-PSDB;
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(UYSH-) UNIV SHEFFIELD
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                                                                                                                                                                                                                                                                                                         Dictyostelium
                                                                                                                                                                                                                                                                                                                              osteoporosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 SMANAGKDTNGSQFFITT 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                     discoideum cyclophilin (DdCyP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates
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                                                           Fig 21; 98pp; English
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3GR, Watts
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                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                          DP1; discoidin II; human DP1; hDP1; cyclophilin; DdCyP2; binding protein; calcium metabolism; cyclosporine; hypercalcaemia; bone metabolism; bone metastases.
                                                                                                                                                                                                                                                                                                        discoideum
                                                                                                                                                                                                                       97US-0039738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ata for this patent did not form part of the printed but was obtained in electronic format directly from
                                                                                                                                                                                                                                           98WO-US02709
                                                                                osteoporosis
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100.0%; Pr
                                                                                                                                                        DJ,
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                                                                                                                                                        Ibbotson KJ,
J, Xiong XJ;
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Pred. No.
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                                                                                          hypercalcaemia,
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3e-09;
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This represents the amino acid sequence of cyclophilin (DdCyP2) from the DictyOstelium discoideum Ax-2. The invention provides sequences encoding DictyOstelium Dp1, human Dp1 (hDP1) and DictyOstelium cyclophilin (DdCyP2) which are bisphosphonate binding proteins. The invention also provides methods for purifying and producing such bisphosphonate binding

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ARG65277
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RESULT 15
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Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a proliferation agent for haematopoietic stem cells, which contains cyclophilin. This may be used in the treatment of dyshaemopolesis in radiotherapy and chemotherapy of various haematopoletic organ diseases and cancers. The present sequence is a human protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haematopoletic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proliferation agent for hematopoietic stem cell containing cyclophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-DEC-1999;
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                          AAG65278;
                                                                      AAG65278 standard;
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                                                                      protein;
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human; mouse.
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2.3e-07;
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. 2.4e-07;
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Search completed: April 10, Job time: 37 secs
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Best Local 9
                                                                                         Matches
                                                                                                                                                       The present invention provides a proliferation agent for haematopoietic stem cells, which contains cyclophilin. This may be used in the treatment of dyshaemopoiesis in radiotherapy and chemotherapy of various haematopoietic organ diseases and cancers. The present sequence is a murine protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                          proliferation agent for hematopoietic stem cell containing cyclophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                           dyshaemopoiesis;
                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                        (KANF ) KANEKA CORP
                                                                                                                                                                                                                                                                                                                               03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                     03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                JP2001163798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Haematopoietic stem cell dyshaemopoiesis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haematopoietic stem
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                                                                                                                                     Sequence
                                                                    85
                                               60 FHRVIKDEMIQGGDFT
                                                                                                    Local Similarity
                                                          FHRVIKDEMIQGGDET
                                                                                                                                                                                                                                                                                   2001-592517/67
                                                                                          16;
                                                                                                                                     185 AA;
                                                                                                                                                                                                                            Page 17; 19pp; Japanese.
                                                                                          Conservative
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human; mouse.
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               11:54:16
                                                                                                     Score 16;
Pred. No.
                                                                                           Mismatches
                                                                                                     DB 22;
2.4e-07;
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                                                                                            0;
                                                                                                               Length 185
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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-482-728A-10
US-08-482-728A-10
US-08-482-728A-97-8
US-08-142-897-8
US-08-142-897-8
US-08-142-897-8
US-08-145-995A-9
US-08-451-747-9
US-08-451-747-14
US-08-145-995A-16
US-08-451-747-14
US-08-145-995A-14
US-08-145-995A-14
US-08-145-995A-14
US-08-145-995A-14
US-08-145-995A-14
US-09-134-852-12
US-08-145-995A-17
US-08-145-995A-17
US-08-145-995A-7
US-08-145-995A-7
US-08-145-995A-7
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Sequence 10, App1
Sequence 11, App1
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Sequence
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US-08-142-897-7
Best Local Similarity
               Query Match
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US-08-451-747-4	US-08-451-747-3	-80-	US-08-145-995A-3	-09-	US-09-134-852-13	US-08-451-747-13	US-08-145-995A-13	US-08-482-728A-14	US-08-482-728A-12	US-09-134-852-15	US-08-451-747-15	ò	-08	-09-134	80-	US-08-145-995A-5	US-09-134-852-7
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                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/142,897
FILING DATE:
CLASSIFICATION NUMBER: US/08/142,897
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/005,917
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: DATA:
APPLICATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 5490A-92-1
TELECHAN: 415-326-2400
TELECHAN: 415-326-2402
                                                                                                                                                                      TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 5447852.
TITLE OF INVENTION: and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                       LENGTH:
                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  STRANDEDNESS:
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5447852el Cyclophilins, Associating Proteins
                                                                                                                                                                                                                                                                             5490A-92-1
Score 208; DB 1;
Pred. No. 1.4e-188;
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               Length 208;
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RESULT 2
US-08-482-728A-10
                                                                                                                                                                                      ; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-482-728A-10
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                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 398
TELEX: 910 277299
INFORMATION FOR SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fisher, Josep APPLICANT: Payan, Donald TITLE OF INVENTION: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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110 IYGERFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKTAMLDGKHVVFGKVLEGME 169
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STATE: California
                                                                                    50 GRVIFGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKS 109
                                                                                                                      Local Similarity
les 126; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                   GRVIFGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGPTTRGDGTGGKS 60
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                                                                                                                                                                                                                                                                          126 amino acids
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                                                                                                                   60.6%; So ilarity 100.0%; I Conservative 0;
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Pred. No. 1.9e-111;
0; Mismatches 0;
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US-08-142-897-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11,
                                                                                                                                                       Sequence 5, Application US/08142897 Patent No. 5447852
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                          GENERAL INFORMATION:
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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SOFTWARE: Pate:...
CURRENT APPLICATION NUMBER: US/08/482,728A
APPLICATION NUMBER: US/08/482,728A
APPLICATION NUMBER: US/08/482,728A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Silva, Robin M.
REGISTATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Silva, Robin M.
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MEDIUM TYPE: Floppy disk
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APPLICANT: Fisher,
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                     APPLICANT: Friedman, Jeffrey S. APPLICANT: Weissman, Irving L. TITLE OF INVENTION: No. 5477852
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MOLECULE TYPE:
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                                                        NUMBER OF SEQUENCES:
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                            83 SKFHRVIKDFMIQGGD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                             34 SKFHRVIKDFMIQGGD
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Four Embarcadero Center,
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                                                                          Irving L.
No. 5447852el Cyclophilins, Associating Proteins
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                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Friedman, Jeffrey S.
APPLICANT: Weissman, Irving L.
TITLE OF INVENTION: No. 547852el Cyclophilins, Associating Proteins
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 10
             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 15-JAN-1993
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/ACENT INFORMATION:
NAME: Dunn, Tracy D.
REGISTRATION NUMBER: 34,587
REGISTRATION NUMBER: 34,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 15-JAN-1993 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION DATA:
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                                                                   APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                       CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 FHRVIKDFMIQGGDFT 102
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California
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One Market Plaza,
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                                                                                                                                        Release #1.0, Version #1.25
                                 US 08/005,917
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Pred. No.
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US-08-482-728A-9
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Best Local Similarity 100.0%;
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
              MOLECULE TYPE:
                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Bruce
APPLICANT: Fisher, Josep
APPLICANT: Payan, Donald
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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TELEPHONE: 415-326-2400
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                                                               TYPE:
                                                                                                                                                                                              NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                TOPOLOGY:
                                           STRANDEDNESS:
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ADDRESSEE: 6 Herbert
STREET: Four Embarcadero Center, Suite 3400
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STRANDEDNESS: sin
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REGISTRATION NUMBER: 34,587
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FILING DATE: 05-AUG-1991
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94111-4187
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                                unknown
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Pred. No.
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Query Match

Best Local Similarity

5.8%; 100.0%;

Score 12; Pred. No.

DB 2;

NUMBER OF SEQUENCES:

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                                                                                                                    US-08-145-995A-9
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                                                                                  sequence 9, Application US/08145995A Patent No. 5482850
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Best Local :
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PRIOR APPLICATION NOMBER: US 08/005,917
APPLICATION NUMBER: US 08/005,917
FILLING DATE: 15-JAN-1993
PRIOR APPLICATION NUMBER: US 07/740,375
FILING DATE: 05-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: DURIN, TEACY D.
REGISTRATION NUMBER: 34,587
REGISTRATION NUMBER: 34,587
                              GENERAL INFORMATION:
APPLICANT: CARLOW, CLOT-
APPLICANT: PAGE, ANTONY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Tracy J. Dunn
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
TITLE OF INVENTION:
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                                                                                                                                                                                    104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                                                                     Local Similarity 100 les 12; Conservative
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                      H: 163 amino acids
amino acid
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                                                  CARLOW, CLOTILDE K.S.
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                                                                                                                                                                                                                                                                   5.8%; Score 12; DB 1; L
100.0%; Pred. No. 0.00074;
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No. 5447852el Cyclophilins, Associating Proteins and Uses
METHOD FOR IDENTIFYING ANTI-PARASITIC COMPOUNDS
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US-08-451-747-9
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TELEPAX: (617) 523-6440
TELEPAX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
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SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,995A
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN;
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 43
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METHOD FOR I
TITLE OF INVENTION: COMPOUNDS
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STRANDEDNESS: un
                                                   APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
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                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                       STATE:
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SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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0.00075;
hes 0;
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CLASSIFICATION:

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US-09-134-852-9
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Best Local Similarity 100.0%;
Matches 12; Conservative
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APPLICANT: CARLOW, CLOT
APPLICANT: PAGE, ANTONY
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SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-554
TELEFAX: (508) 927-1705
                                                                                                                                                   REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-0CT-1993
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE:
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                                STRANDEDNESS:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: BOSTON
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                 TOPOLOGY:
                                                                                                                     TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/134,852
                                                                  LENGTH:
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Pred. No.
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0.00075;
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                                                                                                                RESULT 12
US-08-451-747-8
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US-08-145-995A-8
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                                                                                   Sequence 8, Application US/08451747 Patent No. 5821107
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APPLICANT: CARLOW, CLOT
APPLICANT: PAGE, ANTONY
                                                                      GENERAL INFORMATION:
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TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
         APPLICANT: CARLOW, CLOTI
APPLICANT: PAGE, ANTONY
TITLE OF INVENTION: METH
TITLE OF INVENTION: COM
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NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                          153 WLDGKHVVFGKV 164
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TELEX: 200291 STRE UR
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                                                        CARLOW, CLOTILDE K.S.
                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                            unknown
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METHOD FOR IDENTIFYING ANTI-PARASITIC COMPOUNDS 21
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Pred. No.
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Pred. No
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US-09-134-852-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09134852 Patent No. 6127148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                       APPLICANT: CARLOW, CLOTILDE K.S
APPLICANT: PACE, ANTONY
TITLE OF INVENTION: METHOD FOR
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/1.
FILING DATE: 29-CCT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,852
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEPAX: (508) 927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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OPERATING SYSTEM:
                                                                                                                                                                   ZIP: 02109
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CLASSIFICATION:
                                                                                                                                                                                                                          CITY: BOSTON
                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                          ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 12; DB 2; I
Local Similarity 100.0%; Pred. No. 0.00075;
les 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01915
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32 TOZER ROAD
                                                                                                                                                                                                                                        130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                            CARLOW, CLOTILDE K.S.
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                                               TELEFAX: (41,,99
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEFEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 mnino acids
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                                                                                                                                                          REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
MOLECULE TYPE:
                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Silva, Robin M.
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: protein
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0:
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                  STRANDEDNESS:
                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Four Embarcadero Center, Suite 3400
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RESNICK, DAVID S.
34235
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                    unknown
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; Pred. No. 0.00075;
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COMPUTER READABLE FORM:

COMPUTER TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURERNT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 36-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 398-3249
TELEPAN: (415) 398-3249
TELEEX: 910 277299
INFORMATION FOR SEC ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TVPPE: amino acids
Search completed: April 10, 2003, 11:56:00 Job time: 16 secs
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                                                                                                                               Qy
                                                                                                                                                                                                                                                               ; STRANDEDNESS: unknown; TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-482-728A-13
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US-08-482-728A-13
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Patent No. 5968802
GENERAL INFORMATION:
APPLICANY: Wang, Bruce
APPLICANY: Fisher, Joseph
APPLICANY: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                     Ouery Match 5.3%; Score 11; DB 2; Length 134 Best Local Similarity 100.0%; Pred. No. 0.0055; Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                               139 TNGSQFFITTV 149
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CITY: San Francisco
STATE: California
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ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                  Length 134;
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                  Score
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Match
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208
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/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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      2 US-10-043-142-12

2 US-10-043-142-11

2 US-10-043-142-10

2 US-10-043-142-10

2 US-10-043-142-5

0 US-10-043-142-5

0 US-09-925-300-1279

0 US-09-864-761-40591

US-10-121-049-8

US-10-121-049-8

US-10-123-904-8

US-10-175-746-8

US-10-175-746-8

US-10-176-918-8

US-10-137-965-8

US-10-137-865-8

US-10-140-474-8

US-10-142-431-8

US-10-143-114-8

US-10-143-114-8

US-10-143-114-8

US-10-143-114-8
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Sequence 8, Appli
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                                                                                                                                                                                  Sequence 11, Appl
Sequence 10, Appl
Sequence 5, Appli
Sequence 1279, Ap
Sequence 40591, A
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Sequence 1323, Ap
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US-09-205-658-90	US-09-205-658-61	US-09-864-761-34903	US-09-986-480-195	US-09-864-761-36135	US-09-864-761-45050	US-09-925-442-36	US-09-986-480-402	US-09-468-147-166	US-09-468-147-91	US-09-738-626-4403	US-09-764-870-292	US-10-125-540-292	US-09-815-242-14085	0S-09-815-242-10261	US-09-969-834-4	US-09-949-192-51	US-09-738-626-5320	US-09-738-626-3539	\mathbf{r}	US-10-143-032-8	4		10-142-423-	US-10-123-262-8	US-10-142-419-8	
	Sequence 61, Appl	e 34	Sequence 195, App	Sequence 36135, A	450	Sequence 36, Appl	402,	166	Sequence 91, Appl	Sequence 4403, Ap	e 292	Sequence 292, App		Sequence 10261, A	Sequence 4, Appli	Œ		539	E.	œ	æ	e 8		æ	Sequence 8, Appli	

ALIGNMENTS

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APPLICANT: DERKX, PATRICK M.F.
APPLICANT: MADRID, SUSAN M.
TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
FILE REFERENCE: 078883/0128
CURRENT APPLICATION NUMBER: US/10/043,142
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 09/806.399
PRIOR APPLICATION NUMBER: PT/IE99/01669
PRIOR APPLICATION NUMBER: PT/IE99/01669
PRIOR APPLICATION NUMBER: CB 9821198.0
PRIOR FILING DATE: 1998-09-30
PRIOR FILING DATE: PATENTE PATEN
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LENGTH: 208
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181 SRDKPLKDVIIADCGKIEVEKPFAIAKE 208
                                                                                                                                                                                           121 KLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTD
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                                                                                           KLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTD 180
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181

SRDKPLKDVIIADCGKIEVEKPFAIAKE 208

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GENERAL INFORMATION:
APPLICANT: DERKX, PATRICK M.F.
APPLICANT: MADRID, SUSAN M.
APPLICANT: MADRID, SUSAN M.
TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
FILE REFERENCE: 07883/0128
CURRENT APPLICATION NUMBER: US/10/043,142
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 09/806,399
PRIOR FILING DATE: 1092-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: PCT/IB99/01669
PRIOR APPLICATION NUMBER: PCT/IB99/01669
PRIOR FILING DATE: 1999-09-30
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: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (57)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1323
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US-10-043-142-11
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LENGTH: 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-08-10
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                   PRIOR APPLICATION NUMBER: GB 9821198.0 PRIOR FILING DATE: 1998-09-30 NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
SOFTWARE: PatentIn Ver.
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NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264
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; TYPE: PRT; ORGANISM: Mus musculus US-10-043-142-11
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; ORGANISM: Aspergillus niger
US-10-043-142-5
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LENGTH: 207
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SEQ ID NO 10
LENCTH: 203
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Best Local S
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Patent No. US20020150969A1
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Best Local Similarity
                                                                                      SEQ ID NO 5
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Patent No. US20020150969A1
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APPLICANT: MADRID, SUSAN M.
TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
FILE REFERENCE: 078883/0128
CURRENT APPLICATION NUMBER: US/10/043,142
CURRENT FILING DATE: 2002-01-14
CURRENT FILING DATE: 2002-01-14
                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/043,142
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: 09/806,399
PRIOR FILING DATE: 2002-03-30
PRIOR APPLICATION NUMBER: PCT/IB99/01669
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
                                                                                                                                                                                                                                                                                                                                           APPLICANT: DERKX, PATRICK M.F.
APPLICANT: MADRID, SUSAN M.
TITLE OF INVENTION: PERTIDYL PROLYL CIS-TRANS ISOMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: GB 9
PRIOR FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 12
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PRIOR FILING DATE: 2002-03-30
PRIOR APPLICATION NUMBER: PCT/IB99/01669
PRIOR FILING DATE: 1999-09-30
                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 078883/0128
                                                                                                                             PRIOR FILING DATE: 1998-09-30 NUMBER OF SEQ ID NOS: 12
                                                                                                        SOFTWARE: PatentIn Ver.
                                                                                                                                                                       PRIOR APPLICATION NUMBER: GB 9821198.0
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                                            TYPE: PRT
                                                            LENGTH: 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 GYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity nes 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 GYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERF 109
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1.7e-27;
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US-09-925-300-1279, Application US/09925300

Patent No. US20020151681A1

GENERAL INFORMATION:
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                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR RILING DATE: 2000-10-04
PRIOR RILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
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SEQ ID NO 1279
LENGTH: 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40591, Application US/09864761 Patent No. US20020048763A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENEME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENEME EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/925,300 CURRENT FILING DATE: 2001-08-10 PRIOR APPLICATION NUMBER: PCT/US00/05988 PRIOR FILING DATE: 2000-03-08
                                      PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PA101
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Craig Rosen APPLICANT: Steve Rube
                                                                                                      PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 FHRVIKDFMIQGGDFTRGDGTGGKSIYGE 113
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                   APPLICATION NUMBER: PCT/US01/00664
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ilarity 100.0%;
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Pred. No.
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Pred. No.
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hes 0;
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GENERAL INFORMATION:
APPLICANT: Baker, Kev
APPLICANT: Beresini
APPLICANT: DeForge,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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LENGTH: 108
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APPLICANT:
APPLICANT:
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APPLICANT:
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                             APPLICANT:
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
                                                                    APPLICANT:
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PRIOR FILING DATE: 2001-01-30
   APPLICANT:
                                APPLICANT:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 GTGGKSIYGE 113
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Wood, William
                            Tumas, Daniel
Watanabe, Colin K
                                                                                                                                                                                             Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                           Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                               Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                           Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                               DeForge, Laura
                                                                                             Stewart, Timothy A.
                                                                                                                                 Smith, Victoria
                                                                                                                                                                    Sherwood, Steven
                                                                                                                                                                                                                                                                  Goddard, Audrey
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NN: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

NN: EXPRESSED IN LUNG, SIGNAL = 3.2

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8

NN: EXPRESSED IN HEART, SIGNAL = 3.6

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.6

NN: EXPRESSED IN HELA, SIGNAL = 1.6

NN: EXPRESSED IN HELA, SIGNAL = 1.6

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

NN: EXPRESSED IN HELA, SIGNAL = 1
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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CURRENT APPLICATION NUMBER: US/10/028,072

APPLICANT: Zhang TITLE OF INVENTION:

PRIOR CURRENT OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065846
OR FILING DATE: 1997-11-17
OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/066453
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/066511
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24 OR APPLICATION NUMBER: 60/063082
OR FILING DATE: 1997-10-31
OR APPLICATION NUMBER: 60/063127
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063327
OR FILING DATE: 1997-10-27
OR FILING DATE: 1997-10-27
OR APPLICATION NUMBER: 60/063529
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/06350
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063561
OR APPLICATION NUMBER: 60/063704
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063733
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063735
OR APPLICATION NUMBER: 60/063735
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OR APPLICATION NUMBER: 60/063736
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063736
OR APPLICATION NUMBER: 60/063736
OR APPLICATION NUMBER: 60/063736 OR APPLICATION NUMBER: 60/05958
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/05958
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/059836
OR APPLICATION NUMBER: 60/059836
OR APPLICATION NUMBER: 60/062250
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062287
OR APPLICATION NUMBER: 60/062814
OR APPLICATION NUMBER: 60/062814
OR APPLICATION NUMBER: 60/062814
OR APPLICATION NUMBER: 60/062816
OR APPLICATION NUMBER: 60/063045
OR APPLICATION NUMBER: 60/063045
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063045
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063045 OR APPLICATION NUMBER: 60/059115
OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059117
OR APPLICATION NUMBER: 60/059122
OR APPLICATION NUMBER: 60/059122
OR APPLICATION NUMBER: 60/059184
OR APPLICATION NUMBER: 60/059184
OR FILING DATE: 1997-09-17 NENT FILING DATE: 2001-12-NE APPLICATION NUMBER: 60/0-NE FILING DATE: 1997-06-18 NE APPLICATION NUMBER: 60/0-NE FILING DATE: 1997-08-26 APPLICATION NUMBER: 07.10-17
FILING DATE: 1997-10-17
FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/064248 FILING DATE: 1997-09-17 APPLICATION NUMBER: 60/059263 FILING DATE: 1997-09-18 FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/064809
FILING DATE: 1997-11-07
APPLICATION NUMBER: 60/065186 APPLICATION NUMBER: 60 FILING DATE: 1997-09-2001-12-19 60/059113 9-17 60/056974 60/049911

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OR APPLICATION NUMBER: 60/084627
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084637
OR FILING DATE: 1998-05-12
OR FILING DATE: 1998-05-12
OR APPLICATION NUMBER: 60/085323
OR APPLICATION NUMBER: 60/085323
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085338
OR FILING DATE: 1998-05-13
OR APPLICATION NUMBER: 60/085338
OR APPLICATION NUMBER: 60/085338
OR APPLICATION NUMBER: 60/085338 OR FILING DATE: 1998-02-27
OR APPLICATION NUMBER: 60/07963
OR FILING DATE: 1998-02-27
OR APPLICATION NUMBER: 60/079728
OR APPLICATION NUMBER: 60/08165
OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/081203
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081229
OR APPLICATION NUMBER: 60/08129
OR APPLICATION NUMBER: 60/081695
OR FILING DATE: 1998-04-19
OR APPLICATION NUMBER: 60/081695
OR APPLICATION NUMBER: 60/081817
OR APPLICATION NUMBER: 60/081817
OR APPLICATION NUMBER: 60/081817
OR APPLICATION NUMBER: 60/081817
OR APPLICATION NUMBER: 60/081817 PR FILING DATE: 1998-05-22

REAPPLICATION NUMBER: 60/08

REFLING DATE: 1998-05-22

PR APPLICATION NUMBER: 60/08

REFLING DATE: 1998-05-28

REPLICATION NUMBER: 60/08

REPLICATION NUMBER: 60/08 OR FILING DATE: 1998-03-12
RE APPLICATION NUMBER: 60/07
RE FILING DATE: 1998-03-20
RE FILING DATE: 1998-03-25
RE FILING DATE: 1998-03-25 FILING DATE: 1998-UJ -(APPLICATION NUMBER: 60/0
TITING DATE: 1998-05-15 R APPLICATION NI R FILING DATE: R APPLICATION NI R APPLICATION N R FILING DATE: R APPLICATION N FILING DATE: 1998-05-15
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/ FILING DATE: APPLICATION N APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083545
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/084600 APPLICATION NUMBER: 60/081818 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60 FILING DATE: 1997-12-1 APPLICATION NUMBER: FILING DATE: 1997-12 APPLICATION NUMBER: 60 FILING DATE: 1997-12-1 APPLICATION NUMBER: 60 FILING DATE: 1997-12-APPLICATION APPLICATION N FILING DATE: APPLICATION NUMBER: 60/077791 FILING DATE: NUMBER: 60/085579 NUMBER: 60/082999 NUMBER: NUMBER: NUMBER: NUMBER: NUMBER: 60/088730 1998-05-13 1998-04-24 1998-02-04 1998-02-09 1998-01-23 1997-12-60/088026 60/086430 60/086414 60/085704 60/085697 60/074092 60/069334 60/087106 60/079294 60/078910 60/074086 60/073612 60/072320 60/069694 60/069278 60/069212

FILING DATE: 1998-06-10

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC17
CURRENT APPLICATION NUMBER: U$/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 8
LENGTH: 166
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10121049 Publication No. US20030022239A1 GEMERAL INFORMATION:
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Best Local
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DR FILING DATE: 1998-06-26

DR APPLICATION NUMBER: 60/091360

DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091519

DR APPLICATION NUMBER: 60/091519

DR FILING DATE: 1998-07-02
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FILING DATE: 19/98-06-11
APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090538
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
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Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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APPLICANT:

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RESULT 11
US-10-140-470-8
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US-10-123-904-8
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Best Local S
Matches 10
                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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LENGTH: 166
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Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. Gurney, Austin L. Sherwood, Steven
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                       Gao, Wei-Qiang
                                                                                   Filvaroff, Ellen
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; SEQ ID NO 8
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-8
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; TYPE: PRT
; ORGANISM: HOMO S
US-10-140-470-8
RESULT 13
US-10-176-918-8
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US-10-175-746-8
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Best Local :
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACLDS ENCODING THE SAME
FILE REFERENCE: 9330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 550
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                                                             IKDFMIQGGD 66
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Wood, William
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Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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                                                                                                                           4.8%; Score 10; DB
100.0%; Pred. No. 0.
1ve 0; Mismatches
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0.058;
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US-10-176-921-8
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LENGTH: 166
TYPE: PRT
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            Prior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 8
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File W.
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                                                        APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC288
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
CURRENT FILING DATE: 2002-06-20
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LENGTH: 166
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Godowski, Paul J.
Gurney, Austin L.
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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APPLICANT: TUMBS, DATIEST
APPLICANT: Watenabe, Colin K
APPLICANT: Watenabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT PILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 8
LENCTH: 166
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-865-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10137865
Publication No. US20030032155A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Berosers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Goo, Wei-Qiang
APPLICANT: Goo, Wei-Qiang
APPLICANT: Goodard, Audrey
APPLICANT: Goodowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
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Search completed: April 10, 2003, 11:56:23 Job time : 18 secs
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US-10-137-865-8
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; ORGANISM: Homo Sapien
US-10-176-921-8
                                                                                                                                                                                                    Query Match 4.8%; Score 10; DB 9; Length 166; Best Local Similarity 100.0%; Pred. No. 0.058; Matches 10; Conservative 0; Mismatches 0; Indels
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peptidylprolyl iso
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4 U	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
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S38324	T05766	S30507	T27373	S22496	CSCK	CSZPA	CSBY	в53522	B53422	T50838	T02489	T40819	T50837	S48018	T47724
peptidylprolyl iso	20k cyclophilin -	peptidylprolyl iso													

ALIGNMENTS

A:Molecule type: mRNA
A:Residues: 'MLRLSERN',1-208 <SPI>
A:Residues: 'MLRLSERN',1-208 <SPI>
A:Cross-references: GB:M63573; NID:g33799B; PIDN:AAA36601.1; PID:g337999
A:Cross-references: GB:M63573; NID:g33799B; PIDN:AAA36601.1; PID:g337999
A:Note: the authors' translation begins at an ATG codon in poor context for initiati
A:Note: parts of this sequence, including the amino end of the mature form, were con
R:Mariller, C.; Allain, F.; Kouach, M.; Spik, G.
Biochim. Biophys. Acta 1293, 31-38, 1996
Biochim. Biophys. Acta 1293, 31-38, 1996
Biochim. Biophys. Acta 1293, 31-38, 1996
A:Title: Evidence that human milk isolated cyclophilin B corresponds to a truncated A:Reference number: S65742; MUID:96186273; PMID:8652625
A:Accession: S65742 R;Spik, G.; Haendler, B.; Delmas, O.; Mariller, C.; Chamoux J. Biol. Chem. 266, 10735-10738, 1991
A;Tille: A novel secreted cyclophilin-like protein (SCYLP). A;Reference number: A40515; MUID:91280363; PMID:2040592
A;Accession: A40515 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000 C;Accession: A39118; A39722; A40515; \$65742 R;Price; E.R.; Zydowsky I.D.; Jin, M.; Baker, C.H.; McKeon, F.D.; Walsh, C.T. Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991 Proc. Natl. Acad. Sci. U.S.A. 88, 1903-1907, 1991 A;Title: Human cyclophilin B: a second cyclophilin gene encodes a peptidyl-prolyl ista;Reference number: A39118; MUID:91156714; PMID:2000394 A;Accession: A39118 C; Function: A;Cross-references: GDB:127610; OMIM:123841 A;Map position: 15q21-15q22 A; Gene: GDB: PPIB C;Comment: This protein is distinguished from peptidylprolyl isomerase A by the pres-C;Comment: This protein binds to and is inhibited by the immunosuppressive drug cycle A; Molecule type: protein A; Residues: 26-30; 203 <MAR> A; Experimental source: milk A;Cross-references: GB:M60457; NID:g181249; PIDN:AAA35733.1; R;Spik, G.; Haendler, B.; Delmas, O.; Mariller, C.; Chamoux, A; Title: An endoplasmic reticulum-specific A; Reference number: A39722; MUID:91260697; A; Accession: A39722 A;Cross-references: GB:M60857; NID:g181334; PIDN:AAA52150.1; PID:g181335 R;Hasel, K.W.; Glass, J.R.; Godbout, M.; Sutcliffe, J.G. Mol. Cell. Biol. 11, 3484-3491, 1991 peptidylproly1 isomerase (EC 5.2.1.8) B precursor [validated] - human N;Alternate names: cyclophilin B; cyclosporin A-binding protein B; S-cyclophilin C;Species: Homo sapiens (man) C; Genetics: A; Molecule type: mRNA A; Residues: 1-208 < HAS> A; Residues: 1-208 < PRI> A; Molecule type: mRNA cyclophilin. PMID:1710767 PID:g181250 M.; Maes, P.; initiati

A;Description: catalyzes the cis-trans isomerization of peptidylproline peptide C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase; cyclosporin A binding; glycoprotein; T-cell F;1-25/Domain: signal sequence #status predicted <SIG>

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peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat
N;Alternate names: cyclophilin B; ppTASE
C:SpecLes: Rattus norvegicus (Norway rat)
C;Date: 15-Nov-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: S71547
R;Ruecknagel, K.P.; Pfelfer, T.; Rahfeld, J.U.; Schaerfke, M.; Fischer, G.
submitted to the Protein Sequence Database, November 1996
A;Reference number: S71547
A;Accession: S71547
A;Accession: S71547
A;Accession: S71547
A;Roceule type: protein
A;Residues: 1-183 <RUE>
A;Experimental source: liver
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase
F;1-183/Product: peptidylprolyl isomerase, isoform 20.3K #status experimental ch
                                                                           peptidylprolyl isomerase (EC 5.2.1.8) CyP-S1 precursor - mouse
N;Alternate names: cyclophilin B; cyclophilin-S1; cyclosporin A-binding protein
C:Species: Mus musculus (bouse mouse)
C;Date: 05-Jan-1996 *sequence_revision 05-Jan-1996 *text_change 16-Jul-1999
C;Accession: A56661; B39722; S21835
R;Schumacher, A; Schroter, H; multhaup, G.; Nordhelm, A.
Biophlm. Biophys. Acta 1129, 13-22, 1991
A;Title: Murine cyclophilin-S1: a variant peptidyl-prolyl isomerase with a putative sign A;Accession: A56861; MUID:92096454; PMID:1756174
A;Accession: A56861
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-216 <SCH:
A:Experimental source:
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Best Local
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                      type: mRNA: 1-216 <SCH>
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teratocarcinoma
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Pred. No.
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Pred. No. :
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RESULT 5

peptidylprolyl isomerase (EC 5.2.1.8) B - bovine (1
N;Alternate names: cyclophilin B
C;Species: Bos primigenius taurus (cattle)
C;Date: 25-Dec-1994 #sequence_revision 14-Jul-1995
C;Accession: S45724

(fragment)

#text_change

11-Jun-1999

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A40516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-207 < CAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: S-cyclophilin.
A;Reference number: A40
A;Accession: A40516
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptidylprolyl isomerase (EC 5.2.1.8) (S-cyclophilin) precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #sext_change 16-Jul-1992 #sext_change 16-Jul-1
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A; Residues: 9-216 < NOR>
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A; Residues: 9-216 < HAS>
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A; Title: An endoplasmic reticulum-specific cyclophilin. A; Reference number: A39722; MUID:91260697; PMID:1710767
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                                      114 REPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGM
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                                                                                                                                                                                              Local Similarity
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REPDENEKLKHYGPGWVSMANAGKDTNGSQFEITTVKTAWLDGKHVVEGKVLEGM 167
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100.08;
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B; Pred. No. 8.3
0; Mismatches
                                                                                                                                                        0;
                                                                                                                                                                                              Score 55;
Pred. No.
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peptidylprolyl isomerase (EC,5.2.1.8).F31C3.1 [similarity] - Caenorhabditis elegar

N;Contains: cyclophilin

C:Specles: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000

C;Accession: T21587

R;Cottage, A.

Submitted to the EMBL Data Library, March 1997

A;Reference number: Z19446

A;Accession: T21587

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-204 <WIL>

A;Cross-references: EMBL:292784; PIDN:CAB07192.1; GSPDB:GN00019; CESP:F31C3.1

A;Experimental source: clone F31C3

A;Gene: CESP:F31C3.1

A;Map position: 1

A;Introns: 69/3

C;Superfamily: peptidylprolyl isomerase; cyclophilin homology

C;Reywords: cis-trans:-lsomerase

F;28-190/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptidylprolyl isomerase (EC 5.2.1.8) - Streptomyces chrysomallus N;Alternate names: cyclophilin A; cyclosporin A-binding protein C.Species: Streptomyces chrysomallus C.Species: Streptomyces chrysomallus C.Species: Streptomyces chrysomallus C;Date: 17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change 16-Jul-1999 C;Accession: S28020; S25676 R.Pahl, A.; Uehlein, M.; Bang, H.; Schlumbohm, W.; Keller, U. Mol. Microbiol. 6, 3551-3558, 1992 A;Title: Streptomycetes possess peptidyl-prolyl cis-trans isomerases that strongly resem A;Reference number: S28020; MUID:93116593; PMID:1474897 A;Accession: S28020; MUID:93116593; PMID:1474897 A;Residues: 1-165 <PAH; A;Residues: 1-165 <PAH; A;Cross-references: EMBL-215137; NID:946835; PIDN:CAA78840.1; PID:946836 C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Reywords: cis-trans-isomerase; cyclophilin homology C;Reywords: cis-trans-isomerase; cyclophilin homology CYP>
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A:Accession: $45724
A:Molecule type: protein
A:Residues: 1-46 <GAL>
C:Superfamily: peptidylprolyl isomerase; cyclophilin homology
C:Keywords: cis-trans-isomerase; cyclosporin A binding
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  Query Match
Best Local
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Similarity
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31-36, 1994
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8.2%;
100.0%;
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Pred. No.
Score 17;
Pred. No.
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Pred. No.
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DB 2;
1e-08;
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                   Length 204;
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C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase; cyclosporin A binding F;37-199/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                  Cell 6, 799-806, 1991
A;Title: Two cytoplasmic candidates for immunophilin action are A;Reference number A40047; MUID:91347379; PMID:1652374
A;Accession: A40047
                                                                                                                                                                                                                                                                                                                                       peptidylprolyl isomerase (EC 5.2.1.8) (cyclophilin C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 C;Accession: A40047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase F;25-187/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: cyclophilin
C;Species; Caenorhabditis elegans
C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 02-Sep-2000
                                                                                                                                                A;Cross-references: GB:M74227; NID:g192898; PIDN:AAA37511.1; PID:g192899 C;Comment: This protein binds the immunosuppressive drug cyclosporin A.
                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-212 <FRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, March A; \mbox{Description}: The sequence of C elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-201 < PAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Reference number: 218981
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A; Map position: 3
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A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-201 <TAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z18498
A; Accession: T16351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Taich, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U27354; A;Experimental source: strain N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                   R; Friedman, J.; Weissman,
                                                                                                                                                                                                                                                                                                                                                                                                                             A40047
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                           Score 16;
Pred. No.
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DB 2; 4, 9.9e-08; 0;
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J. 9.5e-08;
J. 0;
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                                             Length 212;
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RESULT 12
T27371
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S46488
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      peptidylproly1 isomerase (EC 5.2.1.8) Y75B12B.2 [similarity] -
N;Contains: cyclophilin
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Contains: cyclophilin
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Jul.1995 *sequence_revision 26-Jul-1996 *text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: peptidylprolyl isomerase; cyclophilin h C;Keywords: cis-trans-isomerase; cyclosporin A binding F;37-199/Domain: cyclophilin homology <CYP>
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                                                                                                                                                                                                                                                                                                                                          C:Superfamily: peptidylprolyl isomerase; cyclophilin homology C:Keywords: cis-trans-isomerase; cyclosporin A binding
                                                                                                                                                                                                                                                                                                                                                                                                                                      Blochem. J. 300, 871-875, 1994
A;Title: The characterization of a cyclophilin-type peptidyl prolyl cis-trans-isomerase
A;Reference number: S46488; MUID:94280416; PMID:8010972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S46488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptldylprolyl isomerase (EC 5.2.1.8) - bovine (fragment) N.Alternate names: peptldylprolyl cis-trans-isomerase
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A;Experimental source: kidney
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A; Residues: 1-212 <SCH>
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  #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
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                                                                                                                                                                                                                                                                                                 Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homology
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                                                                 Caenorhabditis
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peptidylprolyl isomerase (EC 5. N; Alternate names: cyclophilin
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14

1; peptidyl-prolyl cis-trans isomera

isomerase

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R.Page, A.P.; MacNiven, K.
Submitted to the EMBL Data Library,
A:Reference number: Z18986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
T18578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptidylprolyl isomerase (EC 5.2.1.8) c
W;Contains: cyclophilin
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Introns: 23/3; 107/3
C:Superfamily: peptidylprolyl isomerase: cyclophilin
C:Keywords: cis-trans-isomerase
F:3-171/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, October 1995
A;Reference number: Z19867
A;Accession: T24269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-183 <PAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, October 1998 A; Reference number: Z20360 A; Accession: T27371
                                                                                                                                                           C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase
                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-183 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AL032663; PIDN:CAA21760.1; A;Experimental source: clone Y75B12B
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A; Residues: 1-171 <WIL>
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                                                                                                                                          F;16-183/Domain: cyclophilin
                                                                                                                                                                                            A; Introns: 34/3; 87/3; 148/1
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                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                    A; Experimental source:
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                                 FHRVIKDFMIQGGDF
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15; Conserv
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Pred. No.
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                                                                                   DB 2; Le 8.3e-07;
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A;Gene: TP0947
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology C;Keywords: cis-trans-isomerase
F;34-206/Domain: cyclophilin homology <CYP>
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R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidembaram, M.; Utterback, T.; rson, J.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
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Search completed: April 10, 2003, 11:55:39 Job time : 21 secs
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A;Residues: 1-215 <COL>
A;Cross-references: GB:AE001263; GB:AE000520; NID:g3323266; PIDN:AAC65904.1; PID:g332326
A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A71250; MUID:98332770; PMID:9665876 A;Accession: A71261
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C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclosporin A binding
F;3-171/Domain: cyclophilin homology <CYP>
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A;Molecule type; mRNA
A;Residues: 1-172 <SOM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Chlamydomonas reinhardtii C:Date: 21-May-1999 #text_change 08-Oct-1999 C:Accession: T07950 C:Accession: T07950 R:Somanchi, A.; Handley, E.R.; Moroney, J.V.
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A; Accession: T07950
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nes 14; Conserv
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Local Similarity 100.0%; Pred. No. 7.5e-06;
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OM protein - protein search, using sw model
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Run on:

April 10, 2003, 11:52:26 ; Search time 12 Seconds (without alignments) 718.923 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-720-469A-44 208 1 MKVLLAAALIAGSVFFLLLP.....VIIADCGKIEVEKPFAIAKE 208

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4.8	4.8	4.8	4.8	4.8	4.8	4.8				4.00	4.
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CYPM_RAT	CYPM_MOUSE	CYP1_CAEEL	CYPH_MAIZE	CYPH_CATRO	CYP1_ARATH	CYPH_BRANA	CYPZ_MOUSE	CYPZ_HUMAN	CYPH_HEMPU	CYPH_BLAGE	CYPH_ECHGR
P29117 rattus norv		P52009 caenorhabdi			P34790 arabidopsis		Q9d0w5 mus musculu		P91791 hemicentrot		P14088 echinococcu

ALIGNMENTS

RA R	RP RA	RP RA	RESULT CYPB_HI ID C! AC P! DT 0: DT 1: DT 1: DE (II DE (II OC BI OC BI
SUBCELLULAR LOCATION. SUBCELLULAR LOCATION. MEDLINE-92112948; PubMed-1530944; Arber S., Krause KH., Caroni P.; "S-cyclophilin is retained intracellularly via a unique COOH-terminal sequence and colocalizes with the calcium storage protein calrettcuiin."; J. Cell Biol. 116:113-125(1992). MEDLINE-94255495; PubMed-8197205; MEDLINE-94255495; PubMed-8197205; MIKOL V., Kallen J., Walkinshaw M.D.;	SEQUENCE OF 2-208 FROM N.A. MEDLINE=91260697; pubMed=1710767; Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.; "An endoplasmic reticulum-specific cyclophilin."; MOI. Cell. Biol. 11:3484-3491(1991). SEQUENCE OF 64-76 AND 151-157, MEDLINE=93162043; PubMed=1286667; MAD	SEQUENCE FROM N.A., AND SEQUENCE OF 26-40. MEDIJINE-91156714; PubMed-2000394; Price E.R., Zydowsky L.D., Jin M., Hunter C.H., McKeon F.D., Walsh C.T.; "Human cyclophilin B: a second cyclophilin gene encodes a peptidyl- prolyl isomerase with a signal sequence."; Proc. Natl. Acad. Sci. U.S.A. 88:1903-1907(1991). [2] SEQUENCE FROM N.A. MEDIJINE-91250363; PubMed-2040592; Spik G., Heendler B., Delmas O., Mariller C., Chamoux M., Maes P., Tartar A., Montreuil J., Stedman K., Kocher H.P., Keller R., Hiestand P.C., Movva N.R.; "A novel secreted cyclophilin-like protein (SCYLP)."; J. Biol. Chem. 266:10735-10738(1991).	LIT 1 2.HUMAN CYPB.HUMAN STANDARD; PRT; 208 AA. P23284; 01-NCV-1991 (Rel. 20, Created) 01-NCV-1991 (Rel. 20, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase) Peptid OR CYPB. (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1). PPIB OR CYPB. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID-9606;

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RESULT 2
CYPB_M
ID CYPB_M
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EMBL; M63573; AAA36601.1; A
EMBL; M60457; AAA35733.1; A
PIR; A39118; CSHUB.
PIR; A40515; A40515.
Ol-MAR-1992 (Rel. 21, Greater)
Ol-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peppildyl-prolyl cls-trans isomerase B precursor (EC 5.2.1.8) (PPIase)
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                                                                                                                                                                       CYPB_MOUSE
P24369;
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PRINTS; PR00153; CSAPPISMRASE.
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SWISS-2DPAGE; P23284; HUMAN
Aarhus/Ghent-2DPAGE; 117; NI
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Multigene fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:9255; PPIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002130; CSA_PPIase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS SUBCELLULAR LOCATION: Endoplasmic reticulum lume
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligopeptides.
CATALYTIC ACTIVITY: Peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c. Natl. Acad. Sci. U.S.A. 91:5183-5186(1994).
FUNCTION! PPIASES accelerate the folding of proteins.
the cis-trans isomerization of proline imidic peptide
                                                                                                                                                                                                                                                                                                                                   SRDKPLKDVIIADCGKIEVEKPFAIAKE 208
                                                                                                                                                                                                                                                                                                                                                               SRDKPLKDVIIADCGKIEVEKPFAIAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLKHYGPGWVSMANAGKDTNGSOFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKVLLAAALIAGSVFFLLLPGPSAADEKKKGPKYTVKVYFDLRIGDEDVGRVIFGLFGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                         KLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESFKTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKYLLAAALIAGSVFFLLLPGPSAADEKKKGPKVTVKVYFDLRIGDEDVGRVIFGLFGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
199
208 AA;
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ilarity 100.0%;
Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isomerase; Rotamase; Signal; Endoplasmic
                                                                                                                                                                                                      STANDARD;
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208 F
208 F
22742 MW;
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PREVENT SECRETION FROM ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 208; UB _,
No. 8.5e-184;
                                                                                                                                                                                                      PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOMERASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
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RESULT 3
CYPB_BOVIN
ID CYPB_B
AC P80311
DT 01-JUN
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CYPB_BOVIN
P80311;
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
wammaiia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Hasel K.W., Glass J.R., Godbout M., Sutcliffe J.G.
"An endoplasmic reficulum-specific cyclophilin.";
"An endoplasmic reficulum-specific cyclophilin.";
Mol. Cell. Biol. 11:3484-3491(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSA-PFISMRASE_1, 1.
PROSITE; PS50070; CSA_PPIASE_2; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:97750; Ppib.
InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M60456; AAA37498.1; EMBL; X58990; CAA41736.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclosporin; Isomerase; Rotamase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENZYME RÉGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By simi
SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligopeptides.
CATALYTIC ACTIVITY:
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S21835; S21835.
                                                                                                                                                                                                                                                                                                       FGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRCDGTGGKSIYGE
                                                                                                                                                                             RFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKT 151
                                                                                                                                                                                                                           RFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKT 151
                                                                                                                                                                                                                                                                              FGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGE
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                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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199
     (Rel.
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                                                      STANDARD;
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208
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                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 98;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4B8DF5AE40BAD3A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Endoplasmic reticulum;
                                                        208
                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Le
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    peptidylproline

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Best Local :
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                                                                                                                                                                       CONFLICT
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Bose S., Muecke M., Freedman R. B.;
Bose S., Muecke M., Freedman R. B.;
"The characterization of a cyclophilin-type peptidyl prolyl cis-trans-isomerase from the endoplasmic-reticulum lumen.";
Els-trans-isomerase from the endoplasmic-reticulum lumen.";
Blochem. J. 300:871-875(1994).

11-FUNCTION: PPIAses accelerate the folding of proteins. I
                                                                                                                                                                                                     SITE
                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                    PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                 InterPro; IPR002130; CSA_PPIase. Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartiod
                                                                                                                                                                                                                                          Multigene family.
                                                                                                                                                                                                                                                            Cyclosporin;
                                                                                                                                                                                                                                                                                                                                               HSSP; P23284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carrello A., Mark P.J.,
Submitted (JAN-1993) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase B precursor (EC (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP).
                             143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 26-45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cyclophilin-B is an abundant protein whose conformation
to cyclophilin-A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galat A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94283623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 26-71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae;
 143
                                                                                    83
                                                                                                             Local Similarity nes 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENZYME RÉGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligopeptides, CATALYTIC ACTIVITY: Peptidylproline (omega=180) =
                          QFFITTVKTAWLDGKHV 159
                                                                   SKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENFKLKHYGPGWYSMANAGKDTNGS
QFFITTVKTAWLDGKHV
                                                   SKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENFKLKHYGPGWVSMANAGKDTNGS
                                                                                                                                                                                                                                                                                                                                                          D14073; BAA03158.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bouet F
                                                                                                                                                                      30
208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347:31-36(1994).
                                                                                                               Conservative
                                                                                                                                                                                                                                                          Isomerase;
                                                                                                                                                              25
208
208
30
30
22701
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Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                          37.0%;
159
                                                                                                                                                                                                                                                         Rotamase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        House A.K., Ratajczak
the EMBL/GenBank/DDBJ
                                                                                                                                                                       MW:
                                                                                                             0
                                                                                                                          Score 77;
Pred. No.
                                                                                                                                                                  PEPTIDYL-PROLYL CIS-TRANS PREVENT SECRETION FROM ER K -> G (IN REF. 3).
0097C88289AF6276 CRC64;
                                                                                                             Mismatches
                                                                                                                                                                                                                                                    Signal; Endoplasmic reticulum;
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. 1.9e-63;
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                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      roteins. It catalyzes peptide bonds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
cora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptidylproline
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CYPB_CHICK
ID CYPB_C
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                                                                                                                                         RESULT
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Best Local :
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                                                                                           CYPB_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPRO02130; CSA_PPIase. Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92112948; PubMed=1530944;
Arber S., Krause K.-H., Caroni P.;
"S-cyclophilin is retained intracellularly via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase B precursor (EC (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "S-cyclophilin is retained intracellularly via a unique COOH-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cyclosporin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligopeptides.
-- CATALYTIC ACTIVITY: Peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning of a complementary protein mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P23284; 1CYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Cell Biol. 116:113-125(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calreticulin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS TO C-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90300692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                              149
                                                                                                                                                                                                                                                         149 VKT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kidney Int. 37:1460-1465(1990)
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                                                                                                                                            G
                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                      89 IKDFMIQGGDFTRGDGTGGKSIYGERFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Omega=0).

ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPB.
SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By
SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PPIases accelerate the folding of proteins. the cis-trans isomerization of proline imidic peptide
                                                                                                                                                                                                              VKT 151
                                                                                                                                                                                                                                                                                                  IKDFMIQGGDFTRGDGTGGKSIYGERFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITT
                                                                                                                                                                                                                                                                                                                                                                                                  63
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199
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                           STANDARD;
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
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PEPTIDYL-PROLYL CIS-TRANS
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                                                                                         PRT;
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76D12AC3427FEF32 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bonds in
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P24367; 01-MAR-1992 01-MAR-1992 15-JUN-2002

(Rel. (Rel. (Rel.

21, Created)
21, Last sequence up
41, Last annotation

update)

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Best Local
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the secretory pathway.";
J. Blol. Chem. 266:10739-10742(1991).
-i- FUNCTION: PPlases accelerate the folding of proteins.
the cis-trans isomerization of proline imidic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in oway modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                   Q06118;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Peptidyl-prolyl cis-trans isomerase (E
(Cyclophilin homolog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50772; CSA_PPIASE_2; 1.
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SEQUENCE FROM N.A.,
STRAIN-ATCC 11523;
MEDLINE-93116593; P
                                                                                                                                                    Streptomyces chrysomallus
Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                               PPI_STRCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "S-cyclophilin. New member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity). SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligopeptides.
CATALYTIC ACTIVITY: Peptidylproline (omega=180)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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198
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                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                              Streptomycineae;
     PubMed-1474897
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207
207
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                                                    SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MΨ.
                                                                                                                              Actinobacteria (class); Ac
ycineae; Streptomycetaceae;
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Pred. No.
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PEPTIDYL-PROLYL CIS-TR
PREVENT SECRETION FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                 on update)
(EC 5.2.1.8)
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3.1e-4
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s 0;
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bonds in
                                                                                                                                                                                                                                   (Rotamase)
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SAN DE LE RESERVATION DE LE RE
   CYP5_CAEEL
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Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PTISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pahl A., Uehlein M., Bang H., Schlumbohm W., Keller U.;
"Streptomycetes possess peptidy1-prolyl cis-trans isomerases
strongly resemble cyclophilins from eukaryotic organisms.";
MO1. Microbiol. 6:3551-3558(1992).
-1- PUNCTION: PPTases accelerate the folding of proteins. It
the cis-trans isomerization of proline imidic peptide bon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYP5_CAEEL
P52013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Peptidyl-prolyl cis-trans isomerase 5
(Cyclophilin-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclosporin;
SEQUENCE 1
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                                                                                                                                                                                                                                                                                                                                                   MEDLINE-902/0410, Function of the cyclophilin Page A.P., Macniven K., Hengartner M.O.;
"Cloning and biochemical characterization of the cyclophilin "Cloning and biochemical characterization" of the cyclophilin "Cloning and biochemical characterization of the cyclophilin "Cloning and biochemical characterization" of the cyclophilin "Cloning and Cloning and 
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This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinfo
                                                                                                                                                                                                                                                                                                                           homologues from the free-living nematode Biochem. J. 317:179-185(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=96276416; PubMed=8694762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
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PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                     -!- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                               cligopeptides.
CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                     FUNCTION: PPIases accelerate the the cis-trans isomerization of pr
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l Similarity 100.0%;
19; Conservative
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165 AA; 17716 MW;
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(EC 5.2.1.8)
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RESULT 8

CYP6_CAEEL

ID CYP6_C

P52014

AC P52014

AC P52014

DT 01-CCT

DT 01-CCT

DT 01-CCT

CREATY

OC CAENOR

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RN FAGE

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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptilgyl-prolyl cis-trans isomerase 6 precursor
                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPIases accelerate the folding of proteins the cis-trans isomerization of proline imidic peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page A.P., Macniven K., Hengartner M.O.; "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegablochem. J. 317:179-185(1996).
                                                    WormPep; F42G9.2; CE01301.
                                                                          EMBL; U27354; AAC47124.1;
EMBL; U00051; AAA91355.1;
HSSP; P23284; 1CYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol
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STRAIN-Bristol N2;
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PROSITE; PS50072; CSA_PPIASE_2; 1.
ISOMETASE; ROTAMASE; MULTIGENE family.
SEQUENCE 204 AA; 22366 MW; 22ABB39AD1127BAA CRC64;
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                                                                                                                                                                                                                                                                                                             between
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Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMAASE.
                                 InterPro;
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                                                                                                                                                                                send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                         oligopeptides.
CATALYTIC ACTIVITY: Peptidylproline (omega=180) - peptidylproline
                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration reen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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     pro_isomerase;
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CSA_PPIase.
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RESULT 9
CYPC_HUMAN
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D1 15-JUN
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D2 Peptid
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GN PONO S.
OC EUKARY
OC MAMMAI
OX NCBI_T
RN SEDUEN
RX MEDLIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence upda
15-JUN-2002 (Rel. 41, Last annotation up
Peptidyl-prolyl cis-trans isomerase C (E
(Cyclophilin C).
PPIC OR CYPC.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata;
Manmalia; Eutheria; Primates; Catarrhini
                                                                 InterPro; IPR002130; CSA_PPIase Pfam; PF00160; pro_isomerase; 1 PRINTS; PR00153; CSAPPISMASE.
                                                                                                                                                                                                                                                                                       wase by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zurini M.G., Quesniaux V.F., Movva N.R., "Human cyclophilin C: primary structure, determination of binding specificity for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-94304830; PubMed-8031755;
Schneider H., Charara N., Schnitz R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYPC_HUMAN P45877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1;
PROSITE; PS50072; CSA_PPIASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 33:8218-8224(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schneider H.,
Zurini M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isomerase; Rotamase; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS CYPC. SUBCELLULAR LOCATION: CYTOPLASMIC. SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligopeptides.
CATALYTIC ACTIVITY: Peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the cis-trans isomerization of proline
                                                                                                                                             123842;
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                                                                                                                                                                                         S71018; AAB31350
BC002678; AAH026
P05092; 2RMC.
                                                                                                                                                                    HGNC:9256; PPIC
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Pred. No.
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Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           084C5762917F958B CRC64;
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                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wehrli S., Mikol V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
(EC 5.2.1.8)
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2.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (omega=180) = peptidylproline
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                                                                                                                                                                                                                                                                                                                                      Usage
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PROSITE; PS00170; CSA_PPIASE_1; 1. PROSITE; PS50072; CSA_PPIASE_2; 1.

Rotamase; Multigene family.

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RESULT 11
CYP7_CAEEL
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Best Local S
Matches 16
                                                                                                   Query Match
Best Local S
Matches 16
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HSSP: P05092; ZRMC.
MGD: MGI:97751; Ppic.
InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Two cytoplasmic candidates for immu affinity for a new cyclophilin: one absence of CsA.";
Cell 66:799-806(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPTase) (Rotamase)
(Cyclophilin C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                             Pfam: PF00160; pro_isomerase: 1.
PRINTS: PR00153; CSAEPISMRASE:
PROSITE: PS00170; CSA_PPIASE_1: 1.
PROSITE: PS50072; CSA_PPIASE_2: 1.
                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-91347379; PubMed-1652374;
                                                                                                                                                     Cyclosporin; Isomerase; Rotamase; Multigene family, SEQUENCE 212 AA; 22794 MW; C99E7AASDOFA04B6 CRC64;
                                                                                                                                                                                                                                                                    EMBL; M74227; AAA37511.1;
PIR; A40047; A40047.
                                                                                                                                                                                                                                                                                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPIC OR CYPC.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P30412;
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                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligopeptides.
CATALYTIC ACTIVITY: Peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PPIases accelerate the folding the cis-trans isomerization of proline in
                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION: CYCLOSPORIN A (CSA) INHIBITS
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                                                                            FHRVIKDEMIQGGDFT
                                                   FHRVIKDEMIQGGDFT
                                                                                                     16; Conser
                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
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Rodentia;
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                                                                                                   Score 16; DB
Pred. No. 2.2
0; Mismatches
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Pred. No.
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one in the presence
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. 2.2e-07;
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                                                                                                                              DB 1;
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imidic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CYPC
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RESULT 12
CYPB_CAEEL
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STEEN AND DESCRIPTION OF THE PROPERTY OF THE P
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                                                                                                               Query Match
Best Local S
Matches 15
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P52015;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
(Rotamase)
                                                                                                                                                                                                                                 CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97295299; PubMed-9150941;
Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwilling R.;
"Two-dimensional gel electrophoresis of Caenorhabditis elegans
homogenates and identification of protein spots by microsequencing.";
Electrophoresis 18:557-562(1997).
-i- FUNCTION: PPTases accelerate the folding of proteins. It catalvzes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CYP-7 OR Y75B12B.2.
                                                                                                                                                                                                                                                                                                                                                                             Siena-2DPAGE; P52015; ...
wormbep; Y75B12B.2; CE20371.
InterPro; IPR002130; CSA_PPIase.
Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISMAASE.
PRINTS; PR00153; CSAPPISMAASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U27559; AAC47125.1; -. EMBL; AL032663; CAA21760.1; -. HSSP; P05092; 1CWL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page A.P., Macniven K., Hengartner M.O.;
"Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode Caenorhabditis elegation of the cyclophilin homologues from the free-living nematode Caenorhabditis elegations and the cyclophilin homologues. J. 317:179-185(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                           PROSITE: PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - 1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96276416; PubMed=8694762;
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123
                                                         148
                                                                                                                                                                                                                                                                                              (somerase; Rotamase; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligopeptides.
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: PPIases accelerate the folding of proteins, it can the cis-trans isomerization of proline imidic peptide bonds
TVKTAWLDGKHVVFG
                                                      TVKTAWLDGKHVVFG
                                                                                                                                            Similarity
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                                                                                                                                                                                                                                 12
171 AA;
                                                                                                                  Conservative
                                                                                                                                                                                                                              12
18401 MW;
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137
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                                                                                                                                                                                                                                     I -> T (IN REF. 1).
; D5BD5E32A32942A7 CRC64;
                                                                                                                                                                     Score 15;
                                                                                                                  Pred. No. 1.
; Mismatches
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                                                                                                                  1.5e-06;
hes 0;
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                                                                                                                                                                        Length 171;
                                                                                                                     Indels
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Best Local
                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable peptidyl-prolyl cis-trans isomerase
(Rotamase).

Pptn na na---
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase 11 (EC 5.2.1.8) (PPIase)
(Rotamase) (Cyclophilin-11).
CYP-11 OR TOLB7.4.
Treponema pallidum.
Bacteria; Spirochaetales;
                                               PPIB OR PPI OR TP0947.
                                                                                                                                                                                              066105;
                                                                                                                                                                                                                                                TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002130; CSA_PPIase. Pfam; PF00160; pro_isomerase; 1. PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U34955; AAC47115.1; -.
EMBL; Z66499; CAA91297.1; -.
HSSP; P05092; 2CPL.
WormPep; T0187.4; CE03588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way
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"Cloning and biochemical characterization of the cyclophilin monologues from the free-living nematode Caenorhabditis elegans.";
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PROSITE; PS50072; CSA_PPIASE_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
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CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
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15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rotamase;
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                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Multigene family.
20193 MW; 23549C922828C533 CRC64;
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Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No.
                                                                                                                                                                                                                      PRT;
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                                                                                            ion update)
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hes 0;
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Treponema
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 183
                                                                                               5.2.1.8) (PPIase)
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Best Local
                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidy1-prolyl cis-trans isomerase (EC 5.2.1.8)
(Cyclophilin) (Cyclosporin A-binding protein).
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   Eukaryota; Vir
Spermatophyta;
                                                                                                                                                 P34887;
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PRINTS; PR00153; CSAPPISMRASE.
PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                  Allium cepa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                       Isomerase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Nichols;
MEDLINE-98332770; PubMed-9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of homologs for thioredoxin, peptidyl prolyl cis-trans isomerase, and glycerophosphodiester phosphodiesterase in outer membrane fractions from Treponema pallidum, the syphilis spirochete.", Infect. Immun. 65:4179-4189(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL: MEDLINE-97461344; PubMed-9317025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002130; CSA_PPIase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Treponema pallidum, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shevchenko D.V., Akins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=160;
                                                                                                                                                                                                                                             89
                                                                                                                                                                                                                                                                         85 FHRVIKDFMIQGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: PPIases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides (By similarity).

CRTALYIC ACTIVITY: Peptidylproline (omega-180) - peptidylproline
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TP0947; -
                                                                                                                                                                                                                                                                                                                          Similarity
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Viridiplantae; Stro
yta; Magnoliophyta;
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215 AA;
                                  (Onion)
                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                               STANDARD;
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                     ; Complete proteome 23272 MW; CCA1589
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                   Streptophyta;
                                                                                                                                                                                                                                                                                                     Score 14; DB 1; I; Pred. No. 1.5e-05; 0; Mismatches 0;
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Liliopsida; Asparagales;
                                                                                                                                                                                                                                                                                                                                                                   CCA1589C1F5A6D0B CRC64;
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               Embryophyta; Tracheophyta
                                                                                                                                                             ξ
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                                                                                                                                                                                                                                                                                                                                      Length 215
                                                                               (PPIase) (Rotamase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shevchenko
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 Alliaceae;
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CYPB_TAST
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Best Local
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-- FUNCTION: PPIAses accelerate the folding of proteins the cis-trans isomerization of proline imidic peptide oligopeptides.
-- CATALYTIC ACTIVITY: Peptidylproline (omega=180) - pep
STRAIN-S288c / AB972;
MEDLINE-94378003; PubMed-8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston M., Andrews S., Brinkman R., Cooper J., Kirsten J.,
Bu Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase B precursor
(Rotamase) (Cyclophilin B) (Cyclophilin-related
CPR2 OR CYP2 OR SCC2 OR CRG OR YHR057C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                     MEDLINE-90221907; PubMed-2183199;
KOSET P., Sylvester D., Liv1 G.P., Bergsma D.J.;
"A second cyclophilin-related gene in Saccharomyces cerevisiae.";
Nucleic Acids Res. 18:1643-1643(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYPB_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00160; pro_isomerase; 1.
PRINTS; PR00153; CSAPPISHRASE_
PR0SITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; PUDUY4; 4..... Interpro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L13365; AAA32642.1; -. HSSP; P05092; 2CPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 KTAWLDGKHVVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (omega=0).

ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA), CSA MEDIATES
OF ITS EFFECTS VIA AN INHIBITORY ACTION ON PPIASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTAWLDGKHVVFG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Isomerase; Rotamase; Multigene family.
150 AA; 16033 MW; 9223D16840F7E241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162
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Pred. No.
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9.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC 5.2.1.8) (PPIase) protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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SOTTER REPORT TO DESCRIPTION OF THE SECOND CONTRACT OF THE SECOND CO
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Search completed: April 10, Job time : 12 secs
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P23284; 1CYN.
SGD; S0001099; CYP2.
InterPro; IPR002130; CSA_PPIASE.
Pfam; PF00160; Pro_isomerase; 1.
PRINTS; PR00153; CSA_PPIASE_1; 1.
PROSITE; PS00170; CSA_PPIASE_2; 1.
PROSITE; PS500702; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signal sequence.";
Gene 108:73-80(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porter T.G., Levy M.A., Livi Ĝ.P.;
"The CYP2 gene of Saccharomyces cerevisiae encodes a cyclosporin Asensitive peptidyl-prolyl cis-trans isomerase with an N-terminal signal sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its content of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koser P., Bergsma D.J., Cafferkey
Ferrara A., Silverman C., Kasyan K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; x51497; CAA35865.1; ALT_SEQ.
EMBL; U00061; AAB68386.1; -.
PIR; S12324; S12324.
PIR; S46707; S46707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92104509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                             Cyclosporin; Isomerase; Rotamase; Signal; Multigene family. SIGNAL 1 20 OR 34 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                             136
                                                                                                                    137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENZYME REGULATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PPIases accelerate the folding of proteins the cis-trans isomerization of proline imidic peptide
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                                                                                                                 GKDTNGSQFFITT
                                                                                                                                                                             GKDTNGSOFFITT 148
                                                                                                                                                                                                                                   1 Similarity
                                                                                                                                                                                                                                                                                                                                                    21
205 AA;
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=1761234;
                                                                                                                                                                                                                                                                                                                                                    205 I
22769 MW;
                                                                                                                    149
                                                                                                                                                                                                                                                                  6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYCLOSPORIN A (CSA) INHIBITS
                                  2003, 11:54:34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                               Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                    OR 34 (POTENTIAL).

PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; 616EAEB434B37A6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of.
                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                DB 1; Lu.
5. 0.00012;
0;
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Bossard M.J., Johnson R.K.,
                                                                                                                                                                                                                                                                                           Length 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide bonds
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